P 5   OIPE

RAW SEQUENCE LISTING   DATE: 10/04/2001
PATENT APPLICATION: US/09/891,053   TIME: 08:18:55

Input Set : A:\06501-083001.TXT
Output Set: N:\CRF3\10042001\I891053.raw

ENTERED

```
 4  ·110·> APPLICANT: Itadani, Hiraku
 5         Takimura, Tetsuo
 6         Nakamura, Takao
 7         Kobayashi, Masahiko
 8         Tanaka, Ken-ichi
 9         Hidaka, Yusuke
10         Ohta, Masataka
13  ·120·> TITLE OF INVENTION: NOVEL GUANOSINE TRIPHOSPHATE (GTP)
14         BINDING PROTEIN-COUPLED RECEPTOR PROTEINS
17  ·130·> FILE REFERENCE: 06501-083001
19  ·140·> CURRENT APPLICATION NUMBER: 09/891,053
C--> 20 <141> CURRENT FILING DATE: 2001-09-17
22  ·150·> PRIOR APPLICATION NUMBER: PCT/JP99/07280
23  ·151·> PRIOR FILING DATE: 1999-12-24
25  ·150·> PRIOR APPLICATION NUMBER: PCT/JP98/05967
26  ·151·> PRIOR FILING DATE: 1998-12-25
28  ·150·> PRIOR APPLICATION NUMBER: JP 11/145661
29  ·151·> PRIOR FILING DATE: 1999-05-25
31  ·160·> NUMBER OF SEQ ID NOS: 26
33  ·170·> SOFTWARE: FastSEQ for Windows Version 4.0
35  ·210·> SEQ ID NO: 1
36  ·211·> LENGTH: 413
37  ·212·> TYPE: PRT
38  ·213·> ORGANISM: Rattus norvegicus
40  ·400·> SEQUENCE: 1
41 Met Glu Arg Ala Pro Pro Asp Gly Leu Met Asn Ala Ser Gly Thr Leu
42  1               5                   10                  15
43 Ala Gly Glu Ala Ala Ala Ala Gly Gly Ala Arg Gly Phe Ser Ala Ala
44              20                  25                  30
45 Trp Thr Ala Val Leu Ala Ala Leu Met Ala Leu Leu Ile Val Ala Thr
46          35                  40                  45
47 Val Leu Gly Asn Ala Leu Val Met Leu Ala Phe Val Ala Asp Ser Ser
48      50                  55                  60
49 Leu Arg Thr Gln Asn Asn Phe Phe Leu Leu Asn Leu Ala Ile Ser Asp
50 65                  70                  75                  80
51 Phe Leu Val Gly Ala Phe Cys Ile Pro Leu Tyr Val Pro Tyr Val Leu
52              85                  90                  95
53 Thr Gly Arg Trp Thr Phe Gly Arg Gly Leu Cys Lys Leu Trp Leu Val
54          100                 105                 110
55 Val Asp Tyr Leu Leu Cys Ala Ser Ser Val Phe Asn Ile Val Leu Ile
56          115                 120                 125
57 Ser Tyr Asp Arg Phe Leu Ser Val Thr Arg Ala Val Ser Tyr Arg Ala
58      130                 135                 140
59 Gln Gln Gly Asp Thr Arg Arg Ala Val Arg Lys Met Ala Leu Val Trp
60 145                 150                 155                 160
61 Val Leu Ala Phe Leu Leu Tyr Gly Pro Ala Ile Leu Ser Trp Glu Tyr
62              165                 170                 175
```

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```
63 Leu Ser Gly Gly Ser Ser Ile Pro Glu Gly His Cys Tyr Ala Glu Phe
64             180             185             190
65 Phe Tyr Asn Trp Tyr Phe Leu Ile Thr Ala Ser Thr Leu Glu Phe Phe
66             195             200             205
67 Thr Pro Phe Leu Ser Val Thr Phe Phe Asn Leu Ser Ile Tyr Leu Asn
68     210             215             220
69 Ile Gln Arg Arg Thr Arg Leu Arg Leu Asp Gly Gly Arg Glu Ala Gly
70 225             230             235             240
71 Pro Glu Pro Pro Pro Asp Ala Gln Pro Ser Pro Pro Pro Ala Pro Pro
72             245             250             255
73 Ser Cys Trp Gly Cys Trp Pro Lys Gly His Gly Glu Ala Met Pro Leu
74             260             265             270
75 His Ser Ser Gly Ser Ser Ser Arg Gly Thr Glu Arg Pro Arg Ser Leu
76             275             280             285
77 Lys Arg Gly Ser Lys Pro Ser Ala Ser Ser Ala Ser Leu Glu Lys Arg
78     290             295             300
79 Met Lys Met Val Ser Gln Ser Ile Thr Gln Arg Phe Arg Leu Ser Arg
80 305             310             315             320
81 Asp Lys Lys Val Ala Lys Ser Leu Ala Ile Ile Val Ser Ile Phe Gly
82             325             330             335
83 Leu Cys Trp Ala Pro Tyr Thr Leu Leu Met Ile Ile Arg Ala Ala Cys
84             340             345             350
85 His Gly Arg Cys Ile Pro Asp Tyr Trp Tyr Glu Thr Ser Phe Trp Leu
86             355             360             365
87 Leu Trp Ala Asn Ser Ala Val Asn Pro Val Leu Tyr Pro Leu Cys His
88     370             375             380
89 Tyr Ser Phe Arg Arg Ala Phe Thr Lys Leu Leu Cys Pro Gln Lys Leu
90 385             390             395             400
91 Lys Val Gln Pro His Gly Ser Leu Glu Gln Cys Trp Lys
92             405             410
94 <210> SEQ ID NO: 2
95 <211> LENGTH: 1239
96 <212> TYPE: DNA
97 <213> ORGANISM: Rattus norvegicus
99 <220> FEATURE:
100 <221> NAME/KEY: CDS
101 <222> LOCATION: (1)...(1239)
103 <400> SEQUENCE: 2
104 atg gag cgc gcg ccg ccc gac ggg ctg atg aac gcg tcg ggc act ctg      48
105 Met Glu Arg Ala Pro Pro Asp Gly Leu Met Asn Ala Ser Gly Thr Leu
106  1               5              10              15
108 gcc gga gag gcg gcg gct gca ggc ggg gcg cgc ggc ttc tcg gct gcc      96
109 Ala Gly Glu Ala Ala Ala Ala Gly Gly Ala Arg Gly Phe Ser Ala Ala
110             20              25              30
112 tgg acc gct gtc ctg gct gcg ctc atg gcg ctg ctc atc gtg gcc aca     144
113 Trp Thr Ala Val Leu Ala Ala Leu Met Ala Leu Leu Ile Val Ala Thr
114             35              40              45
116 gta ctg ggc aac gcg ctg gtc atg ctc gcc ttc gtg gcg gat tcg agc     192
117 Val Leu Gly Asn Ala Leu Val Met Leu Ala Phe Val Ala Asp Ser Ser
```

```
118       50                    55                    60
120 ctc cgc acc cag aac aac ttc ttt ctg ctc aac ctc gcc atc tcc gac      240
121 Leu Arg Thr Gln Asn Asn Phe Phe Leu Leu Asn Leu Ala Ile Ser Asp
122   65                    70                    75                    80
124 ttc ctc gtg ggt gcc ttc tgc atc cca ttg tac gta ccc tat gtg ctg      288
125 Phe Leu Val Gly Ala Phe Cys Ile Pro Leu Tyr Val Pro Tyr Val Leu
126                 85                    90                    95
128 acc ggc cgt tgg acc ttc ggc cgg ggc ctc tgc aag ctg tgg ctg gtg      336
129 Thr Gly Arg Trp Thr Phe Gly Arg Gly Leu Cys Lys Leu Trp Leu Val
130                 100                   105                   110
132 gta gac tac cta ctg tgt gcc tcc tcg gtc ttc aac atc gta ctc atc      384
133 Val Asp Tyr Leu Leu Cys Ala Ser Ser Val Phe Asn Ile Val Leu Ile
134           115                   120                   125
136 agc tat gac cga ttc ctg tca gtc act cga gct gtc tcc tac agg gcc      432
137 Ser Tyr Asp Arg Phe Leu Ser Val Thr Arg Ala Val Ser Tyr Arg Ala
138       130                   135                   140
140 cag cag ggg gac acg aga cgg gcc gtt cgg aag atg gca ctg gtg tgg      480
141 Gln Gln Gly Asp Thr Arg Arg Ala Val Arg Lys Met Ala Leu Val Trp
142 145                   150                   155                   160
144 gtg ctg gcc ttc ctg ctg tat ggg cct gcc atc ctg agt tgg gag tac      528
145 Val Leu Ala Phe Leu Leu Tyr Gly Pro Ala Ile Leu Ser Trp Glu Tyr
146                 165                   170                   175
148 ctg tct ggt ggc agt tcc atc ccc gag ggc cac tgc tat gct gag ttc      576
149 Leu Ser Gly Gly Ser Ser Ile Pro Glu Gly His Cys Tyr Ala Glu Phe
150                 180                   185                   190
152 ttc tac aac tgg tac ttt ctc atc acg gcc tcc acc ctc gag ttc ttc      624
153 Phe Tyr Asn Trp Tyr Phe Leu Ile Thr Ala Ser Thr Leu Glu Phe Phe
154           195                   200                   205
156 acg ccc ttc ctc agc gtt acc ttc ttc aac ctc agc atc tac ctg aac      672
157 Thr Pro Phe Leu Ser Val Thr Phe Phe Asn Leu Ser Ile Tyr Leu Asn
158       210                   215                   220
160 atc cag agg cgc acc cgc ctt cgg ctt gat ggg ggc cgt gag gct ggc      720
161 Ile Gln Arg Arg Thr Arg Leu Arg Leu Asp Gly Gly Arg Glu Ala Gly
162 225                   230                   235                   240
164 cca gaa ccc cca cca gat gcc cag ccc tcg cca cct cca gct ccc ccc      768
165 Pro Glu Pro Pro Pro Asp Ala Gln Pro Ser Pro Pro Pro Ala Pro Pro
166                 245                   250                   255
168 agc tgc tgg ggc tgc tgg cca aaa ggg cat ggc gag gcc atg ccg ttg      816
169 Ser Cys Trp Gly Cys Trp Pro Lys Gly His Gly Glu Ala Met Pro Leu
170                 260                   265                   270
172 cac agc tct ggc agc tcc tca agg ggc act gag agg cca cgc tca ctc      864
173 His Ser Ser Gly Ser Ser Ser Arg Gly Thr Glu Arg Pro Arg Ser Leu
174           275                   280                   285
176 aaa agg ggc tcc aag cca tca gca tct tca gca tcc ctg gag aag cgc      912
177 Lys Arg Gly Ser Lys Pro Ser Ala Ser Ser Ala Ser Leu Glu Lys Arg
178       290                   295                   300
180 atg aag atg gtg tcc cag agc atc acc cag cgc ttc cgg ctg tcg cgg      960
181 Met Lys Met Val Ser Gln Ser Ile Thr Gln Arg Phe Arg Leu Ser Arg
182 305                   310                   315                   320
```

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/891,053

DATE: 10/04/2001
TIME: 08:18:55

Input Set : A:\06501-083001.TXT
Output Set: N:\CRF3\10042001\I891053.raw

```
184 gac aag aag gtg gcc aag tcg ctg gcc atc atc gtg agc atc ttt ggg    1008
185 Asp Lys Lys Val Ala Lys Ser Leu Ala Ile Ile Val Ser Ile Phe Gly
186             325             330             335
188 ctc tgc tgg gcg ccg tac acg ctc cta atg atc atc cga gct gct tgc    1056
189 Leu Cys Trp Ala Pro Tyr Thr Leu Leu Met Ile Ile Arg Ala Ala Cys
190             340             345             350
192 cat ggc cgc tgc atc ccc gat tac tgg tac gag acg tcc ttc tgg ctt    1104
193 His Gly Arg Cys Ile Pro Asp Tyr Trp Tyr Glu Thr Ser Phe Trp Leu
194             355             360             365
196 ctg tgg gcc aac tcg gcc gtc aac ccc gtc ctc tac cca ctg tgc cac    1152
197 Leu Trp Ala Asn Ser Ala Val Asn Pro Val Leu Tyr Pro Leu Cys His
198     370             375             380
200 tac agc ttc cgc aga gcc ttc acc aag ctc ctc tgc ccc cag aag ctc    1200
201 Tyr Ser Phe Arg Arg Ala Phe Thr Lys Leu Leu Cys Pro Gln Lys Leu
202 385             390             395             400
204 aag gtc cag ccc cac ggc tcc ctg gag cag tgc tgg aag            1239
205 Lys Val Gln Pro His Gly Ser Leu Glu Gln Cys Trp Lys
206             405             410
```

```
209 <210> SEQ ID NO: 3
210 <211> LENGTH: 21
211 <212> TYPE: DNA
212 <213> ORGANISM: Artificial Sequence
214 <220> FEATURE:
215 <223> OTHER INFORMATION: artificially synthesized primer sequence
217 <221> NAME/KEY: misc_feature
218 <222> LOCATION: (1)...(21)
219 <223> OTHER INFORMATION: n = A,T,C or G
221 <400> SEQUENCE: 3
```
W--> 222 batngccaac ctbkccttct c   21
```
224 <210> SEQ ID NO: 4
225 <211> LENGTH: 20
226 <212> TYPE: DNA
227 <213> ORGANISM: Artificial Sequence
229 <220> FEATURE:
230 <223> OTHER INFORMATION: artificially synthesized primer sequence
232 <221> NAME/KEY: misc_feature
233 <222> LOCATION: (1)...(20)
234 <223> OTHER INFORMATION: n = A,T,C or G
236 <400> SEQUENCE: 4
```
W--> 237 ccataaaagn nggggttgac   20
```
239 <210> SEQ ID NO: 5
240 <211> LENGTH: 2700
241 <212> TYPE: DNA
242 <213> ORGANISM: Rattus norvegicus
244 <220> FEATURE:
245 <221> NAME/KEY: CDS
246 <222> LOCATION: (351)...(1589)
248 <221> NAME/KEY: misc_feature
249 <222> LOCATION: (1)...(2700)
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RAW SEQUENCE LISTING   DATE: 10/04/2001
PATENT APPLICATION: US/09/891,053   TIME: 08:18:55

Input Set : A:\06501-083001.TXT
Output Set: N:\CRF3\10042001\I891053.raw

```
250 <223> OTHER INFORMATION: n = A,T,C or G
252 <400> SEQUENCE: 5
253 aattcggcac gagcgggcag atcgcggggc gcactcggtt gcgcgctgag ctaggggtgc      60
254 accgacgcac cgcgggcggc tggagctcgg ctttgctctc gctgcagcag ccgcgccgcc     120
255 cgccccactc cgctcagatt ccgacaccag cccctctgg atcgccctcc tggactctag      180
256 cccgggctct tgctccgacc ccgcggacca tgctccgggc gccccccgga aaaccgggct     240
257 gggcgaagag ccggcaaaga ttaggctcac gagcggggc cccacccggc cacccagctc      300
258 tccgcccgtg ccctgcccgg gtccccgag ccgtgtgagc ctgctgggcc atg gag        356
259                                                       Met Glu
260                                                        1
262 cgc gcg ccg ccc gac ggg ctg atg aac gcg tcg ggc act ctg gcc gga     404
263 Arg Ala Pro Pro Asp Gly Leu Met Asn Ala Ser Gly Thr Leu Ala Gly
264         5                   10                  15
266 gag gcg gcg gct gca ggc ggg gcg cgc ggc ttc tcg gct gcc tgg acc     452
267 Glu Ala Ala Ala Ala Gly Gly Ala Arg Gly Phe Ser Ala Ala Trp Thr
268         20                  25                  30
270 gct gtc ctg gct gcg ctc atg gcg ctg ctc atc gtg gcc aca gta ctg     500
271 Ala Val Leu Ala Ala Leu Met Ala Leu Leu Ile Val Ala Thr Val Leu
272 35                  40                  45                  50
274 ggc aac gcg ctg gtc atg ctc gcc ttc gtg gcg gat tcg agc ctc cgc     548
275 Gly Asn Ala Leu Val Met Leu Ala Phe Val Ala Asp Ser Ser Leu Arg
276                 55                  60                  65
278 acc cag aac aac ttc ttt ctg ctc aac ctc gcc atc tcc gac ttc ctc     596
279 Thr Gln Asn Asn Phe Phe Leu Leu Asn Leu Ala Ile Ser Asp Phe Leu
280                 70                  75                  80
282 gtg ggt gcc ttc tgc atc cca ttg tac gta ccc tat gtg ctg acc ggc     644
283 Val Gly Ala Phe Cys Ile Pro Leu Tyr Val Pro Tyr Val Leu Thr Gly
284             85                  90                  95
286 cgt tgg acc ttc ggc cgg ggc ctc tgc aag ctg tgg ctg gtg gta gac     692
287 Arg Trp Thr Phe Gly Arg Gly Leu Cys Lys Leu Trp Leu Val Val Asp
288         100                 105                 110
290 tac cta ctg tgt gcc tcc tcg gtc ttc aac atc gta ctc atc agc tat     740
291 Tyr Leu Leu Cys Ala Ser Ser Val Phe Asn Ile Val Leu Ile Ser Tyr
292 115                 120                 125                 130
294 gac cga ttc ctg tca gtc act cga gct gtc tcc tac agg gcc cag cag     788
295 Asp Arg Phe Leu Ser Val Thr Arg Ala Val Ser Tyr Arg Ala Gln Gln
296                 135                 140                 145
298 ggg gac acg aga cgg gcc gtt cgg aag atg gca ctg gtg tgg gtg ctg     836
299 Gly Asp Thr Arg Arg Ala Val Arg Lys Met Ala Leu Val Trp Val Leu
300             150                 155                 160
302 gcc ttc ctg ctg tat ggg cct gcc atc ctg agt tgg gag tac ctg tct     884
303 Ala Phe Leu Leu Tyr Gly Pro Ala Ile Leu Ser Trp Glu Tyr Leu Ser
304             165                 170                 175
306 ggt ggc agt tcc atc ccc gag ggc cac tgc tat gct gag ttc ttc tac     932
307 Gly Gly Ser Ser Ile Pro Glu Gly His Cys Tyr Ala Glu Phe Phe Tyr
308         180                 185                 190
310 aac tgg tac ttt ctc atc acg gcc tcc acc ctc gag ttc ttc acg ccc     980
311 Asn Trp Tyr Phe Leu Ile Thr Ala Ser Thr Leu Glu Phe Phe Thr Pro
312 195                 200                 205                 210
```

Use of n and / or Xaa has been detected in the
Sequence Listing. Review the Sequence Listing
to ensure a corresponding explanation is present
in the <220> to <223> fields of each sequence
using n or Xaa.

VERIFICATION SUMMARY   DATE: 10/04/2001
PATENT APPLICATION: US/09/891,053   TIME: 08:18:56

Input Set : **A:\06501-083001.TXT**
Output Set: **N:\CRF3\10042001\I891053.raw**

L:20 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:222 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3
L:237 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4
L:383 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5
L:455 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:11
L:823 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:22
L:838 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:23